Figure 1 BLOSUM62 Substitution Matrix

	C	S	T	P	A	G	N	D	E	Q	H	R	K	M	I	L	V	F	Y	W
C	**9**	-1	-1	-3	0	-3	-3	-3	-4	-3	-3	-3	-3	-1	-1	-1	-1	-2	-2	-2
S	-1	**4**	1	-1	1	0	1	0	0	0	-1	-1	0	-1	-2	-2	-2	-2	-2	-3
T	-1	1	**4**	1	-1	1	0	1	0	0	0	-1	0	-1	-2	-2	-2	-2	-2	-3
P	-3	-1	1	**7**	-1	-2	-1	-1	-1	-1	-2	-2	-1	-2	-3	-3	-2	-4	-3	-4
A	0	1	-1	-1	**4**	0	-1	-2	-1	-1	-2	-1	-1	-1	-1	-1	-2	-2	-2	-3
G	-3	0	1	-2	0	**6**	-2	-1	-2	-2	-2	-2	-2	-3	-4	-4	0	-3	-3	-2
N	-3	1	0	-2	-2	0	**6**	1	0	0	-1	0	0	-2	-3	-3	-3	-3	-2	-4
D	-3	0	1	-1	-2	-1	1	**6**	2	0	-1	-2	-1	-3	-3	-4	-3	-3	-3	-4
E	-4	0	0	-1	-1	-2	0	2	**5**	2	0	0	1	-2	-3	-3	-3	-3	-2	-3
Q	-3	0	0	-1	-1	-2	0	0	2	**5**	0	1	1	0	-3	-2	-2	-3	-1	-2
H	-3	-1	0	-2	-2	-2	1	1	0	0	**8**	0	-1	-2	-3	-3	-2	-1	2	-2
R	-3	-1	-1	-2	-1	-2	0	-2	0	1	0	**5**	2	-1	-3	-2	-3	-3	-2	-3
K	-3	0	0	-1	-1	-2	0	-1	1	1	-1	2	**5**	-1	-3	-2	-3	-3	-2	-3
M	-1	-1	-1	-2	-1	-3	-2	-3	-2	0	-2	-1	-1	**5**	1	2	-2	0	-1	-1
I	-1	-2	-2	-3	-1	-4	-3	-3	-3	-3	-3	-3	-3	1	**4**	2	1	0	-1	-3
L	-1	-2	-2	-3	-1	-4	-3	-4	-3	-2	-3	-2	-2	2	2	**4**	3	0	-1	-2
V	-1	-2	-2	-2	0	-3	-3	-3	-2	-2	-3	-3	-2	1	3	1	**4**	-1	-1	-3
F	-2	-2	-2	-4	-2	-3	-3	-3	-3	-3	-1	-3	-3	0	0	0	-1	**6**	3	1
Y	-2	-2	-2	-3	-2	-3	-2	-3	-2	-1	2	-2	-2	-1	-1	-1	-1	3	**7**	2
W	-2	-3	-3	-4	-3	-2	-4	-4	-3	-2	-2	-3	-3	-1	-3	-2	-3	1	2	**11**

Figure 2. Blast alignment of Pfu (query 1) against Deep Vent (subject 1)

```
>gi|2494186|sp|Q51334|DPOL_PYRSD   DNA polymerase (Deep Vent DNA polymerase)
[Contains: Endonuclease
           PI-PspI (Psp-GDB pol intein)]
          Length = 1312

 Score =  816 bits (2109), Expect = 0.0
 Identities = 414/493 (83%), Positives = 459/493 (92%)

Query: 1    MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHG 60
            MILD DYITE+GKP+IR+FKKENG+FK+E+DR FRPYIYALL+DDS+I+EV+KIT ERHG
Sbjct: 1    MILDADYITEDGKPIIRIFKKENGEFKVEYDRNFRPYIYALLKDDSQIDEVRKITAERHG 60

Query: 61   KIVRIVDVEKVEKKFLGKPITVWKLYLEHPQDVPTIREKVREHPAVVDIFEYDIPFAKRY 120
            KIVRI+D EKV KKFLG+PI VW+LY EHPQDVP IR+K+REH AV+DIFEYDIPFAKRY
Sbjct: 61   KIVRIIDAEKVRKKFLGRPIEVWRLYFEHPQDVPAIRDKIREHSAVIDIFEYDIPFAKRY 120

Query: 121  LIDKGLIPMEGEEELKILAFDIETLYHEGEEFGKGPIIMISYADENEAKVITWKNIDLPY 180
            LIDKGLIPMEG+EELK+LAFDIETLYHEGEEF KGPIIMISYADE EAKVITWK IDLPY
Sbjct: 121  LIDKGLIPMEGDEELKLLAFDIETLYHEGEEFAKGPIIMISYADEEEAKVITWKKIDLPY 180

Query: 181  VEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLTIGRDGSEPK 240
            VEVVSSEREMIKRFL++IREKDPD+I+TYNGDSFD PYL KRAEKLGIKL +GRDGSEPK
Sbjct: 181  VEVVSSEREMIKRFLKVIREKDPDVIITYNGDSFDLPYLVKRAEKLGIKLPLGRDGSEPK 240

Query: 241  MQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWE 300
            MQR+GDMTAVE+KGRIHFDLYHVI RTINLPTYTLEAVYEAIFGKPKEKVYA EIA+AWE
Sbjct: 241  MQRLGDMTAVEIKGRIHFDLYHVIRRTINLPTYTLEAVYEAIFGKPKEKVYAHEIAEAWE 300

Query: 301  SGENLERVAKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRK 360
            +G+ LERVAKYSMEDAK TYELG+EF PME QLSRLVGQPLWDVSRSSTGNLVEW+LLRK
Sbjct: 301  TGKGLERVAKYSMEDAKVTYELGREFFPMEAQLSRLVGQPLWDVSRSSTGNLVEWYLLRK 360

Query: 361  AYERNEVAPNKPSEEEYQRRLRESYTGGFVKEPEKGLWENIVYLDFRALYPSIIITHNVS 420
            AYERNE+APNKP E EY+RRLRESY GG+VKEPEKGLWE +V LDFR+LYPSIIITHNVS
Sbjct: 361  AYERNELAPNKPDEREYERRLRESYAGGYVKEPEKGLWEGLVSLDFRSLYPSIIITHNVS 420

Query: 421  PDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQKIKTKMKETQDPIEKILL 480
            PDTLN EGC+ YD+AP+VGHKFCKD PGFIPSLL  LL+ERQ+IK KMK ++DPIEK +L
Sbjct: 421  PDTLNREGCREYDVAPEVGHKFCKDFPGFIPSLLKRLLDERQEIKRKMKASKDPIEKKML 480

Query: 481  DYRQKAIKLLANS 493
            DYRQ+AIK+LANS
Sbjct: 481  DYRQRAIKILANS 493
```

Figure 2--continued. Blast alignment of Pfu (query 1) against Deep Vent (subject 1)

```
 Score =  473 bits (1216), Expect = e-133
 Identities = 248/283 (87%), Positives = 269/283 (94%)

Query: 492  NSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLYIDTDGLYATIPG 551
            NS+YGYYGYAKARWYCKECAESVTAWGR+YIE V KELEEKFGFKVLYIDTDGLYATIPG
Sbjct: 1029 NSYYGYYGYAKARWYCKECAESVTAWGREYIEFVRKELEEKFGFKVLYIDTDGLYATIPG 1088

Query: 552  GESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEI 611
             + EEIKKKALEFV YIN+KLPGLLELEYEGFY RGFFVTKK+YA+IDEEGK+ITRGLEI
Sbjct: 1089 AKPEEIKKKALEFVDYINAKLPGLLELEYEGFYVRGFFVTKKKYALIDEEGKIITRGLEI 1148

Query: 612  VRRDWSEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPL 671
            VRRDWSEIAKETQA+VLE ILKHG+VEEAV+IVKEV +KL+ YEIPPEKL IYEQITRPL
Sbjct: 1149 VRRDWSEIAKETQAKVLEAILKHGNVEEAVKIVKEVTEKLSKYEIPPEKLVIYEQITRPL 1208
```

```
Query: 672  HEYKAIGPHVAVAKKLAAKGVKIKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAE 731
            HEYKAIGPHVAVAK+LAA+GVK++PGMVIGYIVLRGDGPIS RAILAEE+D +KHKYDAE
Sbjct: 1209 HEYKAIGPHVAVAKRLAARGVKVRPGMVIGYIVLRGDGPISKRAILAEEFDLRKHKYDAE 1268

Query: 732  YYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWLNIKK 774
            YYIENQVLPAVLRILE FGYRKEDLR+QKT+Q GLT+WLNIKK
Sbjct: 1269 YYIENQVLPAVLRILEAFGYRKEDLRWQKTKQTGLTAWLNIKK 1311
```

Figure 3. Assembly of the oligonucleotides into library fragments.

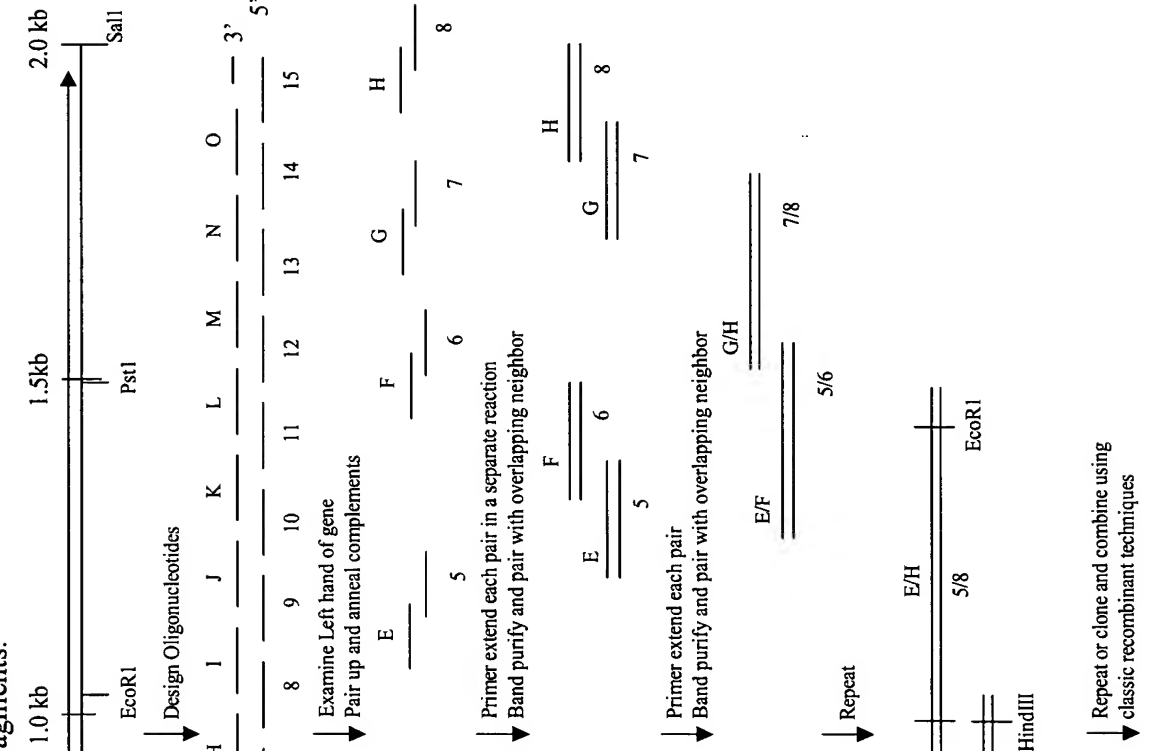


FIG. 4

E coli dut polypeptide sequence:
MKKIDVKILDPRVGKEFPLPTYATSGSAGLDLRACLNDAVELAPGDTTLVPTGLAIHIADPSLAAMMLPRSGLGHKHG
IVLGNLVGLIDSDYQGQLMISVWNRGQDSFTIQPGERIAQMIFVPVVQAEFNLVEDFDATDRGEGGFGHSGRQ

AAD polypeptide sequence:
MSKVILKIKRLPHAQDLPLPSYATPHSSGLDLRAAIEKPLKIKPFERVLIPTGLILEIPEGYEGQVRPRSGLAWKKGL
TVLNAPGTIDADYRGEVKVILVNLGNEEVVIERGERIAQLVIAPVQRVEVVEVEEVSQTQRGEGGFGSTGTK

Alignment:

Identities = 61/149 (40%), Positives = 91/149 (60%), Gaps = 1/149 (0%)

```
Query: 1   MKKIDVKILDPRVGKEFPLPTYATSGSAGLDLRACLNDAVELAPGDTTLVPTGLAIHIAD 60
           M K+ +KI      ++  PLP+YAT  S+GLDLRA +    +++ P +  L+PTGL + I +
Sbjct: 1   MSKVILKIKRLPHAQDLPLPSYATPHSSGLDLRAAIEKPLKIKPFERVLIPTGLILEIPE 60

Query: 61  PSLAAMMLPRSGLGHKHGIVLGNLVGLIDSDYQGQLMISVWNRGQDSFTIQPGERIAQMI 120
                + PRSGL  K G+ + N  G ID+DY+G++ + + N G +    I+ GERIAQ++
Sbjct: 61  -GYEGQVRPRSGLAWKKGLTVLNAPGTIDADYRGEVKVILVNLGNEEVVIERGERIAQLV 119

Query: 121 FVPVVQAEFNLVEDFDATDRGEGGFGHSG 149
             PV + E    VE+    T RGEGGFG +G
Sbjct: 120 IAPVQRVEVVEVEEVSQTQRGEGGFGSTG 148
```

FIGURE 5

5A. Aligned parental sequence showing all possible codons

ECD	1	M	K	K	I	D	V	K	I	L	D	P	R	V	G	K	E	F	P	L	P	T	Y	A	T	S	G	S	A	G	L
		ATG	AAA	AAA	ATT	GAT	GTG	AAA	ATT	CTG	GAT	CCG	CGT	GTG	GGC	AAA	GAA	TTT	CCG	CTG	CCG	ACC	TAT	GCG	ACC	AGC	GGC	AGC	GCG	GGC	CTG
			AAG	AAG	ATC	GAC	GTT	AAG	ATC	TTA	GAC	CCT	CGC	GTT	GGT	AAG	GAG	TTC	CCT	TTA	CCT	ACG	TAC	GCC	ACG	TCT	GGT	TCT	GCC	GGT	TTA
					ATA		GTC		ATA	TTG		CCA	CGG	GTC	GGG				CCA	TTG	CCA	ACT		GCA	ACT	AGT	GGG	AGT	GCA	GGG	TTG
							GTA			CTT		CCC	CGA	GTA	GGA				CCC	CTT	CCC	ACA		GCT	ACA	TCA	GGA	TCA	GCT	GGA	CTT
										CTC			AGA							CTC						TCC		TCC			CTC
										CTA			AGG							CTA						TCG		TCG			CTA

AAD	1	M	S	K	V	I	L	K	I	K	R	L	P	H	A	Q	D	L	P	L	P	S	Y	A	T	P	H	S	S	G	L
		ATG	AGC	AAA	GTG	ATT	CTG	AAA	ATT	AAA	CGT	CTG	CCG	CAT	GCG	CAG	GAT	CTG	CCG	CTG	CCG	AGC	TAT	GCG	ACC	CCG	CAT	AGC	AGC	GGC	CTG
			TCT	AAG	GTT	ATC	TTA	AAG	ATC	AAG	CGC	TTA	CCT	CAC	GCC	CAA	GAC	TTA	CCT	TTA	CCT	TCT	TAC	GCC	ACG	CCT	CAC	TCT	TCT	GGT	TTA
			AGT		GTC	ATA	TTG		ATA		CGG	TTG	CCA		GCA			TTG	CCA	TTG	CCA	AGT		GCA	ACT	CCA		AGT	AGT	GGG	TTG
			TCA		GTA		CTT				CGA	CTT	CCC		GCT			CTT	CCC	CTT	CCC	TCA		GCT	ACA	CCC		TCA	TCA	GGA	CTT
			TCC				CTC				AGA	CTC						CTC		CTC		TCC						TCC	TCC		CTC
			TCG				CTA				AGG	CTA						CTA		CTA		TCG						TCG	TCG		CTA

5B. The minimal encoding sequence

Min. E. Seq.	ATG	AAA	AAA	ATT	GAT	GTG	AAA	ATT	CTG	GAT	CCG	CGT	GTT	GGC	AAA	GAA	TTT	CCG	CTG	CCG	ACC	TAT	GCG	ACC	TCT	GGC	AGC	GCA	GGC	CTG
		GC		G	AT	C			AA	CG	T	C	CA	C	C	T	A				G				C	CA		T		
	M	K	K	I	D	V	K	I	L	D	P	R	V	G	K	E	F	P	L	P	T	Y	A	T	S	G	S	A	G	L
		S		V	I	L			K	R	L	P	H	A	Q	D	L				S				P	H		S		
		R			V				Q	G			D													D				
		N			N				M	H			L													R				

5C. A minimal encoding sequence after the removal of non-similar degeneracies; selection of ADD parent residues at particular sites

	ATG	AAA	AAA	ATT	GAT	GTG	AAA	ATT	CTG	**CGT**	CCG	CGT	**CAT**	GGC	AAA	GAA	TTT	CCG	CTG	CCG	ACC	TAT	GCG	ACC	TCT	**CAC**	AGC	GCA	GGC	CTG
		GC		G	AT	C			AA		T	C		C	C	T	A				G				C			T		
	M	K	K	I	D	V	K	I	L	**R**	P	R	**H**	G	K	E	F	P	L	P	T	Y	A	T	S	**H**	S	A	G	L
		S		V	I	L			K		L	P		A	Q	D	L				S				P			S		
		R			V				Q																					
		N			N				M																					

5A.--continued

ECD	31	D	L	R	A	C	L	N	D	A	V	E	L	A	P	G	D	T	T	L	V	P	T	G	L	A	I	H	I	A	D	P
		GAT	CTG	CGT	GCG	TGC	CTG	AAC	GAT	GCG	GTG	GAA	CTG	GCG	CCG	GGC	GAT	ACC	ACC	CTG	GTG	CCG	ACC	GGC	CTG	GCG	ATT	CAT	ATT	GCG	GAT	CCG
		GAC	TTA	CGC	GCC	TGT	TTA	AAT	GAC	GCC	GTT	GAG	TTA	GCC	CCT	GGT	GAC	ACG	ACG	TTA	GTT	CCT	ACG	GGT	TTA	GCC	ATC	CAC	ATC	GCC	GAC	CCT
			TTG	CGG	GCA		TTG			GCA	GTC		TTG	GCA	CCA	GGG		ACT	ACT	TTG	GTC	CCA	ACT	GGG	TTG	GCA	ATA		ATA	GCA		CCA
			CTT	CGA	GCT		CTT			GCT	GTA		CTT	GCT	CCC	GGA		ACA	ACA	CTT	GTA	CCC	ACA	GGA	CTT	GCT				GCT		CCC
			CTC	AGA			CTC						CTC							CTC					CTC							
			CTA	AGG			CTA						CTA							CTA					CTA							

AAD	31	D	L	R	A	A	I	E	K	P	L	K	I	K	P	F	E	R	V	L	I	P	T	G	L	I	L	E	I	P	E	G
		GAT	CTG	CGT	GCG	GCG	ATT	GAA	AAA	CCG	CTG	AAA	ATT	AAA	CCG	TTT	GAA	CGT	GTG	CTG	ATT	CCG	ACC	GGC	CTG	ATT	CTG	GAA	ATT	CCG	GAA	GGC
		GAC	TTA	CGC	GCC	GCC	ATC	GAG	AAG	CCT	TTA	AAG	ATC	AAG	CCT	TTC	GAG	CGC	GTT	TTA	ATC	CCT	ACG	GGT	TTA	ATC	TTA	GAG	ATC	CCT	GAG	GGT
			TTG	CGG	GCA	GCA	ATA			CCA	TTG		ATA		CCA			CGG	GTC	TTG	ATA	CCA	ACT	GGG	TTG	ATA	TTG		ATA	CCA		GGG
			CTT	CGA	GCT	GCT				CCC	CTT				CCC			CGA	GTA	CTT		CCC	ACA	GGA	CTT		CTT			CCC		GGA
			CTC	AGA							CTC							AGA		CTC					CTC		CTC					
			CTA	AGG							CTA							AGG		CTA					CTA		CTA					

5B--continued

Min. Seq.	GAT	CTG	CGT	GCG	TGC	CTT	AAC	GAT	GCG	GTG	GAA	CTT	GCG	CCG	GGT	GAT	ACG	ACG	CTG	GTT	CCG	ACC	GGC	CTG	GCC	ATT	CAT	ATT	GCG	GAT	CCT
					GC	A	G	G	A	A	C	C	A	A	AA		TT		A	G	GT		A				AT	C	G	A		C		A	GG
	D	L	R	A	C	L	N	D	A	V	E	L	A	P	G	D	T	T	L	V	P	T	G	L	A	I	H	I	A	D	P
					A	I	E	K	P	L	K	I	K		F	E	R	V		I					I	L	E		P	E	G
					S		K	N					E		V			M							V		D				R
					G		D	E					T		C			A							T		Q				A

5C--continued

	GAT	CTG	CGT	GCG	TGC	CTT	AAC	AAT	GCG	GTG	GAA	CTT	GCG	CCG	GGT	GAT	ACG	ACG	CTG	GTT	CCG	ACC	GGC	CTG	**ATC**	ATT	CAT	ATT	GCG	GAT	**GGT**
					GC	A	G	G	A	C	C	A	A	AA		TT		A	G	GT		A					C	G	A		C		A	
	D	L	R	A	C	L	N	D	A	V	E	L	A	P	G	D	T	T	L	V	P	T	G	L	**I**	I	H	I	A	D	**G**
					A	I	E	K	P	L	K	I	K		F	E	R	V		I						L	E		P	E	
					S		K						E		V			M									D				
					G		D						T		C			A									Q				

5A--continued

ECD	62	S	L	A	A	M	M	L	P	R	S	G	L	G	H	K	H	G	I	V	L	G	N	L	V	G	L	I	D	S	D	Y
		AGC	CTG	GCG	GCG	ATG	ATG	CTG	CCG	CGT	AGC	GGC	CTG	GGC	CAT	AAA	CAT	GGC	ATT	GTG	CTG	GGC	AAC	CTG	GTG	GGC	CTG	ATT	GAT	AGC	GAT	TAT
		TCT	TTA	GCC	GCC			TTA	CCT	CGC	TCT	GGT	TTA	GGT	CAC	AAG	CAC	GGT	ATC	GTT	TTA	GGT	AAT	TTA	GTT	GGT	TTA	ATC	GAC	TCT	GAC	TAC
		AGT	TTG	GCA	GCA			TTG	CCA	CGG	AGT	GGG	TTG	GGG				GGG	ATA	GTC	TTG	GGG		TTG	GTC	GGG	TTG	ATA		AGT		
		TCA	CTT	GCT	GCT			CTT	CCC	CGA	TCA	GGA	CTT	GGA				GGA		GTA	CTT	GGA		CTT	GTA	GGA	CTT			TCA		
		TCC	CTC					CTC		AGA	TCC		CTC								CTC			CTC			CTC			TCC		
		TCG	CTA					CTA		AGG	TCG		CTA								CTA			CTA			CTA			TCG		

AAD	62	Y	-	E	G	Q	V	R	P	R	S	G	L	A	W	K	K	G	L	T	V	L	N	A	P	G	T	I	D	A	D	Y
		TAT		GAA	GGC	CAG	GTG	CGT	CCG	CGT	AGC	GGC	CTG	GCG	TGG	AAA	AAA	GGC	CTG	ACC	GTG	CTG	AAC	GCG	CCG	GGC	ACC	ATT	GAT	GCG	GAT	TAT
		TAC		GAG	GGT	CAA	GTT	CGC	CCT	CGC	TCT	GGT	TTA	GCC		AAG	AAG	GGT	TTA	ACG	GTT	TTA	AAT	GCC	CCT	GGT	ACG	ATC	GAC	GCC	GAC	TAC
					GGG		GTC	CGG	CCA	CGG	AGT	GGG	TTG	GCA				GGG	TTG	ACT	GTC	TTG		GCA	CCA	GGG	ACT	ATA		GCA		
					GGA		GTA	CGA	CCC	CGA	TCA	GGA	CTT	GCT				GGA	CTT	ACA	GTA	CTT		GCT	CCC	GGA	ACA			GCT		
								AGA		AGA	TCC		CTC						CTC			CTC											
								AAG		AGG	TCG		CTA						CTA			CTA											

5B--continued

Min. Seq.	TCT	CTG	GCG	GCG	ATG	ATG	CTG	CCG	CGT	AGC	GGC	CTG	GGC	CAT	AAA	CAT	GGC	ATA	GTG	CTG	GGG	AAC	CTG	GTG	GGC	CTG	ATT	GAT	AGC	GAT	TAT
	A	---	A	G	CA	G	G						C	TGG		A G		T	AC	G	CT		GC	CC		AC			GC		
	S	L	A	A	M	M	L	P	R	S	G	L	G	H	K	H	G	I	V	L	G	N	L	V	G	L	I	D	S	D	Y
	Y	-	E	G	Q	V	R						A	W		K		L	T	V	L		A	P		T			A		
					K									R		Q			A		V		P	A		P			T		
					L									Q,Y,*		N			M		R		V	L		M			G		

5C--continued

	TCT	---	GCG	GCG	**CAG**	ATG	CTG	CCG	CGT	AGC	GGC	CTG	GGC	**TGG**	AAA	CAT	GGC	ATA	GTG	CTG	**CTG**	AAC	**GCG**	GTG	GGC	CTG	ATT	GAT	AGC	GAT	TAT
	A		A	G		G	G						C			A G		T	AC	G				CC		AC			GC		
	S	-	A	A	**Q**	M	L	P	R	S	G	L	G	**W**	K	H	G	I	V	L	**L**	N	**A**	V	G	L	I	D	S	D	Y
	Y		E	G		V	R						A			K		L	T	V				P		T			A		
																Q			A					A		P			T		
																N			M					L		M			G		

5A--continued

ECD	93	Q	G	Q	L	M	I	S	V	W	N	R	G	Q	D	S	F	T	I	Q	P	G	E	R	I	A	Q	M	I	F	V	P
		CAG	GGC	CAG	CTG	ATG	ATT	AGC	GTG	TGG	AAC	CGT	GGC	CAG	GAT	AGC	TTT	ACC	ATT	CAG	CCG	GGC	GAA	CGT	ATT	GCG	CAG	ATG	ATT	TTT	GTG	CCG
		CAA	GGT	CAA	TTA		ATC	TCT	GTT		AAT	CGC	GGT	CAA	GAC	TCT	TTC	ACG	ATC	CAA	CCT	GGT	GAG	CGC	ATC	GCC	CAA		ATC	TTC	GTT	CCT
			GGG		TTG		ATA	AGT	GTC			CGG	GGG			AGT		ACT	ATA		CCA	GGG		CGG	ATA	GCA			ATA		GTC	CCA
			GGA		CTT			TCA	GTA			CGA	GGA			TCA		ACA			CCC	GGA		CGA		GCT					GTA	CCC
					CTC			TCC				AGA				TCC								AGA								
					CTA			TCG				AAG				TCG								AGG								

AAD	92	R	G	E	V	K	V	I	L	V	N	L	G	N	E	E	V	V	I	E	R	G	E	R	I	A	Q	L	V	I	A	P
		CGT	GGC	GAA	GTG	AAA	GTG	ATT	CTG	GTG	AAC	CTG	GGC	AAC	GAA	GAA	GTG	GTG	ATT	GAA	CGT	GGC	GAA	CGT	ATT	GCG	CAG	CTG	GTG	ATT	GCG	CCG
		CGC	GGT	GAG	GTT	AAG	GTT	ATC	TTA	GTT	AAT	TTA	GGT	AAT	GAG	GAG	GTT	GTT	ATC	GAG	CGC	GGT	GAG	CGC	ATC	GCC	CAA	TTA	GTT	ATC	GCC	CCT
		CGG	GGG		GTC		GTC	ATA	TTG	GTC		TTG	GGG				GTC	GTC	ATA		CGG	GGG		CGG	ATA	GCA		TTG	GTC	ATA	GCA	CCA
		CGA	GGA		GTA		GTA		CTT	GTA		CTT					GGA	GTA			CGA	GGA		CGA		GCT		CTT	GTA		GCT	CCC
		AGA							CTC			CTC									AGA			AGA				CTC				
		AAG							CTA			CTA									AGG			AGG				CTA				

5B--continued

Min. Seq.	CAG	GGC	CAA	CTG	ATG	ATT	AGC	GTG	TGG	AAC	CGG	GGC	CAG	GAT	TCA	TTT	ACG	ATT	CAG	CCG	GGC	GAA	CGT	ATT	GCG	CAG	ATG	ATT	TTT	GTG	CCG
	G		G	G	A	G	T	C	GT		T		A C	A	GA	G	GT		G	G							C	G	A	C	
	Q	G	Q	L	M	I	S	V	W	N	R	G	Q	D	S	F	T	I	Q	P	G	E	R	I	A	Q	M	I	F	V	P
	R		E	V	K	V	I	L	N		L		N	E	E	V	V		E	R							L	V	I	A	
									L				H		A		M														
									G				K		*		A														

5C--continued

	CAG	GGC	CAA	CTG	ATG	ATT	AGC	GTG	**GTG**	AAC	CGG	GGC	CAG	GAT	**GAA**	TTT	ACG	ATT	CAG	CCG	GGC	GAA	CGT	ATT	GCG	CAG	ATG	ATT	TTT	GTG	CCG
	G		G	G	A	G	T	C			T		A C	A		G	GT		G	G							C	G	A	C	
	Q	G	Q	L	M	I	S	V	**N**	N	R	G	Q	D	**E**	F	T	I	Q	P	G	E	R	I	A	Q	M	I	F	V	P
	R		E	V	K	V	I	L			L		N	E		V	V		E	R							L	V	I	A	
													H				M														
													K				A														

5A--continued

ECD	123	V	V	Q	A	E	F	N	L	V	E	D	F	D	A	T	D	R	G	E	G	G	F	G	H	S	G	R	Q	150
		GTG	GTG	CAG	GCG	GAA	TTT	AAC	CTG	GTG	GAA	GAT	TTT	GAT	GCG	ACC	GAT	CGT	GGC	GAA	GGC	GGC	TTT	GGC	CAT	AGC	GGC	CGT	CAG	
		GTT	GTT	CAA	GCC	GAG	TTC	AAT	TTA	GTT	GAG	GAC	TTC	GAC	GCC	ACG	GAC	CGC	GGT	GAG	GGT	GGT	TTC	GGT	CAC	TCT	GGT	CGC	CAA	
		GTC	GTC		GCA				TTG	GTC					GCA	ACT		CGG	GGG		GGG	GGG		GGG		AGT	GGG	CGG		
		GTA	GTA		GCT				CTT	GTA					GCT	ACA		CGA	GGA		GGA	GGA		GGA		TCA	GGA	CGA		
									CTC									AGA								TCC		AGA		
									CTA									AGG								TCG		AGG		

AAD	122	V	Q	R	V	E	V	V	E	V	E	E	V	S	Q	T	Q	R	G	E	G	G	F	G	S	T	G	T	K	149
		GTG	CAG	CGT	GTG	GAA	GTG	GTG	GAA	GTG	GAA	GAA	GTG	AGC	CAG	ACC	CAG	CGT	GGC	GAA	GGC	GGC	TTT	GGC	AGC	ACC	GGC	ACC	AAA	
		GTT	CAA	CGC	GTT	GAG	GTT	GTT	GAG	GTT	GAG	GAG	GTT	TCT	CAA	ACG	CAA	CGC	GGT	GAG	GGT	GGT	TTC	GGT	TCT	ACG	GGT	ACG	AAG	
		GTC		CGG	GTC		GTC	GTC		GTC			GTC	AGT		ACT		CGG	GGG		GGG	GGG		GGG	AGT	ACT	GGG	ACT		
		GTA		CGA	GTA		GTA	GTA		GTA			GTA	TCA		ACA		CGA	GGA		GGA	GGA		GGA	TCA	ACA	GGA	ACA		
				AGA										TCC				AGA							TCC					
				AGG										TCG				AGG							TCG					

5B--continued

Min. Seq.	GTG	GTG	CAG	GCG	GAA	TTT	AAT	CTG	GTG	GAA	GAT	TTT	GAT	GCG	ACC	GAT	CGT	GGC	GAA	GGC	GGC	TTT	GGC	CAT	AGC	GGC	AGA	CAG	TAA	TGA
		CA	G	T		G	GT	GA			A	G	TC	CA		C	G								TC	C		C	A		
	V	V	Q	A	E	F	N	L	V	E	D	F	D	A	T	D	R	G	E	G	G	F	G	H	S	G	R	Q	*	*
		Q	R	V		V	V	E			E	V	S	Q		Q								S	T		T	K		
		E					I	Q					A	E		E								P						
		L					D	V					Y	P		H								Y						

5C--continued

	GTG	GTG	CAG	GCG	GAA	TTT	AAT	CTG	GTG	GAA	GAT	TTT	**TCT**	**CAG**	ACC	GAT	CGT	GGC	GAA	GGC	GGC	TTT	GGC	**TCT**	AGC	GGC	AGA	CAG	TAA	TGA
		CA	G	T		G	GT	GA			A	G				C	G									C		C	A		
	V	V	Q	A	E	F	N	L	V	E	D	F	**S**	**Q**	T	D	R	G	E	G	G	F	G	**S**	S	G	R	Q	*	*
		Q	R	V		V	V	E			E	V				Q									T		T	K		
		E					I	Q								E														
		L					D	V								H														

FIGURE 6

```
        KpnI  HindIII  NdeI
1   TT GGTACC AAGCTT CAT ATG A(A/G)(A/C) AAA (A/G)TT (G/A)(A/T)T (G/C)TG AAA 38
    AA CCATGG TTCGAA GTA TAC T(T/C)(T/G) TTT (T/C)AA (C/T)(T/A)A (C/G)AC TTT
                          M    K/S/R/N    K    I/V     D/I/V/N     V/L    K

39  ATT (C/A)(T/A)G CGT C(C/T)G C(G/C)T CAT G(G/C)C (A/C)AA GA(A/T) TT(T/A)  69
    TAA (G/T)(A/T)C GCA G(G/A)C G(C/G)A GTA C(C/G)G (T/G)TT CT(T/A) AA(A/T)
     I    L/K/Q/M    R    P/L     R/P    H    G/A      K/Q    E/D    F/L

                                                          StuI
70  CCG CTG CCG A(C/G)C TAT GCG ACC (T/C)CT CAC AGC (G/T)CA GGC CTG GAT CTG 113
    GGC GAC GGC T(G/C)G ATA CGC TGG (A/G)GA GTG TCG (C/A)GT CCG GAC CTA GAC
     P   L   P    T/S    Y   A   T    S/P    H   S    A/S    G   L   D   L

114 CGT GCG (T/G)(G/C)C (C/A)TT (A/G)A(C/G) (A/G)A(T/A) (G/C)CG (G/C)TG (G/A)AA
   140
    GCA CGC (A/C)(C/G)G (G/T)AA (T/C)T(G/C) (T/G)T(A/T) (C/G)GC (C/G)AC (C/T)TT
     R   A    C/A/S/G     L/I     N/E/K/D     D/K/N/E     A/P    V/L     E/K

141 (C/A)TT (G/A)(C/A)G CCG (G/T)(G/T)T GA(T/A) A(C/G)G (A/G)(C/T)G CTG     164
    (G/T)AA (C/T)(G/T)C GGC (C/A)(C/A)A CT(A/T) T(G/C)C (T/C)(G/A)C GAC
      L/I     A/K/E/T    P    G/F/V/C     D/E     T/R     T/V/M/A    L

                AgeI
165 (G/A)TT CCG ACC GGT CTG ATC (A/C)TT (C/G)A(T/A) ATT (G/C)CG GA(T/A) GGT 200
    (C/T)AA GGC TGG CCA GAC TAG (T/G)AA (G/C)T(A/T) TAA (C/G)GC CT(A/T) CCA
      V/I    P   T   G   L   I    I/L     H/E/D/Q    I    A/P     D/E    G

201 T(C/A)T G(C/A)G G(C/G)G CAG (A/G)TG C(T/G)G CCG CGT AGC GGC CTG G(G/C)C 236
    A(G/T)A C(G/T)C C(G/C)C GTC (T/C)AC G(A/C)C GGC GCA TCG CCG GAC C(C/G)G
      S/Y     A/E     A/G    Q    M/V     L/R    P   R   S   G   L    G/A

237 TGG AAA (C/A)A(T/G) GGC (A/T)TA (G/A)(T/C)G (C/G)TG CTG AAC GCG         266
    ACC TTT (G/T)T(A/C) CCG (T/A)AT (C/T)(A/G)C (G/C)AC GAC TTG CGC
     W   K    H/K/Q/N    G    I/L     V/T/A/M     L/V    L   N   A

                          ClaI
267 (G/C)(T/C)G GGC (C/A)(T/C)G ATC GAT (A/G)(G/C)C GAT TAT C(A/G)G GGC     296
    (C/G)(A/G)C CCG (G/T)(A/G)C TAG CTA (T/C)(C/G)G CTA ATA G(T/C)C CCG
      V/P/A/L    G    L/T/P/M    I   D    S/A/T/G    D   Y    Q/R    G

297 (C/G)AA (C/G)TG A(T/A)G (A/G)TT A(G/T)C (G/C)TG GTG AAC C(G/T)G GGC     326
    (G/C)TT (G/C)AC T(A/T)C (T/C)AA T(C/A)G (C/G)AC CAC TTG G(C/A)C CCG
      Q/E     L/V     M/K     I/V     S/I     V/L    N   N    R/L    G

327 (C/A)A(G/C) GA(T/A) GAA (T/G)TT (A/G)(C/T)G ATT (C/G)AG C(C/G)G GGC GAA 356
    (G/T)T(C/G) CT(A/T) CTT (A/C)AA (T/C)(G/A)C TAA (G/C)TC G(G/C)C CCG CTT
      Q/N/H/K     D/E    E    F/V     T/V/M/A    I    Q/E     P/R    G   E

        FspI
357 CGT ATT GCG CAG (A/C)TG (A/G)TT (T/A)TT G(T/C)G CCG GTG (G/C)(T/A)G     389
    GCA TAA CGC GTC (T/G)AC (T/C)AA (A/T)AA C(A/G)C GGC CAC (C/G)(A/T)C
     R   I   A   Q    M/L     I/V     F/I     V/A    P   V    V/Q/E/L

390 C(A/G)G G(C/T)G GAA (T/G)TT (A/G)(A/T)T (C/G)(T/A)G GTG GAA GA(T/A)     416
    G(T/C)C C(G/A)C CTT (A/C)AA (T/C)(T/A)A (G/C)(A/T)C CAC CTT CT(A/T)
      Q/R     A/V    E    F/V     N/V/I/D     L/E/Q/V    V   E    D/E

417 (T/G)TT TCT CAG ACC (G/C)A(T/G) CGT GGC GAA GGC GGC TTT GGC TCT A(G/C)C 458
    (A/C)AA AGA GTC TGG (C/G)T(A/C) GCA CCG CTT CCG CCG AAA CCG AGA T(C/G)G
      F/V    S   Q   T    D/Q/E/H    R   G   E   G   G   F   G   S   S/T

                                BamHI  EcoRI
459 GGC A(G/C)A (C/A)AG TAA TGA GGATCC GAATTC TT                         487
    CCG T(C/G)T (G/T)TC ATT ACT CCTAGG CTTAAG AA
     G    R/T     Q/K    *   *
```

Figure 7

```
        10         20         30         40         50         60         70
TTGGTACCAAGCTTCATATGARMAAARTTRWTSTGAAAATTMWGCGTCYGCSTCATGSCMAAGAWTTWCC
AACCATGGTTCGAAGTATACTYKTTTYAAYWASACTTTTAAKWCGCAGRCGSAGTACSGKTTCTWAAWGG

        80         90        100        110        120        130        140
GCTGCCGASCTATGCGACCYCTCACAGCKCAGGCCTGGATCTGCGTGCGKSCMTTRASRAWSCGSTGRAA
CGACGGCTSGATACGCTGGRGAGTGTCGMGTCCGGACCTAGACGCACGCMSGKAAYTSYTWSGCSACYTT

       150        160        170        180        190        200        210
MTTRMGCCGKKTGAWASGRYGCTGRTTCCGACCGGTCTGATCMTTSAWATTSCGGAWGGTTMTGMGGSGC
KAAYKCGGCMMACTWTSCYRCGACYAAGGCTGGCCAGACTAGKAASTWTAASGCCTWCCAAKACKCCSCG

       220        230        240        250        260        270        280
AGRTGCKGCCGCGTAGCGGCCTGGSCTGGAAAMAKGGCWTARYGSTGCTGAACGCGSYGGGCMYGATCGA
TCYACGMCGGCGCATCGCCGGACCSGACCTTTKTMCCGWATYRCSACGACTTGCGCSRCCCGKRCTAGCT

       290        300        310        320        330        340        350
TRSCGATTATCRGGGCSAASTGAWGRTTAKCSTGGTGAACCKGGGCMASGAWGAAKTTRYGATTSAGCSG
AYSGCTAATAGYCCCGSTTSACTWCYAATMGSACCACTTGGMCCCGKTSCTWCTTMAAYRCTAASTCGSC

       360        370        380        390        400        410        420
GGCGAACGTATTGCGCAGMTGRTTWTTGYGCCGGTGSWGCRGGYGGAAKTTRWTSWGGTGGAAGAWKTTT
CCGCTTGCATAACGCGTCKACYAAWAACRCGGCCACSWCGYCCRCCTTMAAYWASWCCACCTTCTWMAAA

       430        440        450        460        470        480
CTCAGACCSAKCGTGGCGAAGGCGGCTTTGGCTCTASCGGCASAMAGTAATGAGGATCCGAATTCTT
GAGTCTGGSTMGCACCGCTTCCGCCGAAACCGAGATSGCCGTSTKTCATTACTCCTAGGCTTAAGAA
```

Figure 8.

14

atg atc ctg gat g(t/c)t gac tac atc act gaa ga(a/c) ggc aaa ccg (g/a)tt atc cgt (c/a)t(g/c) ttc
M I L D V/A D Y I T E E/D G K P V/I I R L/I/**M** F

aaa aaa gag aac ggc (a/g)aa ttt aag (a/g)tt gag (c/t)at gat cgc a(a/c)c ttt cgt cca tac att tac gct
K K E N G K/E F K I/V E H/Y D R N/T F R P Y I Y A

ctg ctg a(g/a)a gat gat tct (a/c)ag att ga(g/t) gaa gtt a(g/a)a aaa atc act g(g/c)t gag cgc cat ggc aag att
L L R/K D D S K/Q I E/D E V K/R K I T G/A E R H G
K I

214 215

gtt cgt atc (a/g)tt gat g(t/c)g gaa aag gta (g/a)(g/a)g aag aaa ttt ctg ggc a(a/g)a cca atc (a/g)(a/c)g
V R I I/V D V/A E K V **G/E/R/K** K K F L G K/R P I
K/T/E/A

gtg tgg a(g/a)a ctg tat (c/t)tc gaa cat cca caa gat gtt ccg a(t/c)t att cgc ga(g/t) aaa (g/a)tt cgc
V W K/R L Y L/F E H P Q D V P T/A I R E/D K V/I R

gaa cat (c/t)ct gca gtt (g/a)tt gac atc ttc gaa tac gat att cca ttt gca aag cgt tac ctc atc gac aaa
E H P/S A V V/I D I F E Y D I P F A K R Y L I D K

ggc ctg ata cca atg gag ggc ga(g/t) gaa gaa ctc aag (a/c)tc ctg gcg ttc gat ata gaa acc ctc tat
G L I P M E G E/D E E L K I/L L A F D I E T L Y

cac gaa ggc gaa gag ttt g(g/c)t aaa ggc cca att ata atg att agc tat gca gat gaa (a/g)a(a/c) gaa gca aag
H E G E E F G/A K G P I I M I S Y A D E **K/N/E/D** E A
K

gtg att act tgg aaa aa(a/c) ata gat ctc cca tac gtt gag gtt gta tct tcc gag cgc gag atg att aag cgc
V I T W K K/N I D L P Y V E V V S S E R E M I K R

ttt ctc a(g/a)a (g/a)tt atc cgc gag aag gat ccg gac (g/a)tt atc (g/a)tt act tat aac ggc gac tct ttt
F L R/k V/I I R E K D P D V/I I V/I T Y N G D S F

gac (c/t)tc cca tat ctg g(t/c)g aaa cgc gca gaa aaa ctc ggt att aaa ctg (a/c)ct (a/c)tc ggc cgt gat ggt
D F P Y L V/A K R A E K L G I K L T/P I/L G R D
G

tcc gag ccg aag atg cag cgt (a/c)tc ggc gat atg acc gct gta gaa (g/a)tt aag ggt cgt atc cat ttc gac
S E P K M Q R I/L G D M T A V E V/I K G R I H F D

ctg tat cat gta att (a/c)(c/g)c cgt act att aac ctc ccg act tac act ctc gag gct gta tat gaa gca att
L Y H V I T/**S**/**P**/R R T I N L P T Y T L E A V Y E A I

ttt ggt aag ccg aag gag aag gta tac gcc (g/c)at gag att gca (a/g)ag gcg tgg gaa (a/t)cc ggt (a/g)ag
F G K P K E K V Y A D/H E I A K/E A W E T/S G K/E

(a/g)(a/g)c ctc gag cgt gtt gca aaa tac tcc atg gaa gat gca aag g(t/c)g act tat gaa ctc ggc a(g/a)a gaa ttc
N/G/**D**/**S** L E R V A K Y S M E D A K V/A T Y E L G R/K
E F

(c/t)tc cca atg gaa (a/g)(t/c)t cag ctc tct cgc ctg gtt ggc caa cca ctg tgg gat gtt tct cgt tct tcc
L/F P M E I/**T**/**V**/A Q L S R L V G Q P L W D V S R S S

acc ggt aac ctc gta gag tgg t(t/a)t ctc ctg cgc aaa gcg tac gaa cgc aac gaa (g/c)tg gct ccg aac aag
T G N L V E W F/Y L L R K A Y E R N E V/L A P N K

cca (t/g)(c/a)c gaa (c/g)(g/a)a gag tat (c/g)aa cgc cgt ctc cgc gag tct tac (a/g)ct ggt ggc t(t/a)t
P S/**Y**/**A**/D E R/**Q**/**G**/E E Y Q/E R R L R E S Y T/A G G F/Y

gtt aaa gag cca gaa aag ggc ctc tgg gaa (a/g)(a/g)c (a/c)tc gtg t(c/a)c ctc gat ttt cgc (g/t)ct ctg
V K E P E K G L W E N/**S**/**D**/G I/L V Y/S L D F R A/S L

tat ccg tct att atc att acc cac aac gtg tct ccg gat act ctc aac c(t/g)c gag ggc tgc a(g/a)a
Y P S I I I T H N V S P D T L N L/R E G C K/R

(a/g)a(a/c) tat gat (g/a)tt gct ccg (c/g)aa gta ggc cac aag ttc tgc aag gac (a/t)tc ccg ggc ttt att
K/N/E/**D** Y D V/I A P Q/E V G H K F C K D I/F P G F I

ccg tct ctc ctg (a/g)(a/g)g c(a/g)t ctg ctc ga(g/t) gaa cgc caa (a/g)ag att aag (a/c)(g/c)c aaa atg aag
P S L L K/**R**/**E**/G R/H L L E/D E R Q K/E I K T/**S**/**P**/R K M K

g(a/c)g (a/t)cc (c/a)ag gat ccg att gaa aaa a(t/a)a (a/c)tg ctc gac tat cgc caa a(g/a)a gcg att aaa
E/A T/S Q/K D P I E K I/K M/L L D Y R Q R/K A I K

(a/c)tc ctc gca aac tct t(a/t)t tac ggc tat tat ggc tat gca aaa gca cgc tgg tac tgt aag gag tgt gct
L/I L A N S F/Y Y G Y Y G Y A K A R W Y C K E C A

gag tcc gtt act gct tgg ggt cgc (a/g)aa tac atc gag (c/t)tc gtg (t/c)gg aag gag ctc gaa gaa aag ttt ggc
E S V T A W G R K/E Y I E L/F V W/R K E L E E K F G

ttt aaa gtt ctc tac att gac act gat ggt ctc tat gcg act att ccg ggt g(g/c)t (a/g)ag (c/t)ct gag
F K V L Y I D T D G L Y A T I P G G/A E/K S/P E

1696

gaa att aag aaa aag gct ctc gaa ttt gtg **aaa** tac att aac (g/t)cg aag ctc ccg ggt ctc ctg gag ctc gaa
E I K K K A L E F V K(D) Y I N A/S K L P G L L E L E

tat gaa ggc ttt tat (g/a)(t/a)g cgc ggc ttc ttc gtt acc aag aag a(g/a)a tat gcg (g/c)tg att gat gaa gaa
Y E G F Y V/**E**/**M**/K R G F F V T K K R/K Y A V/L I D E E

ggc aaa (g/a)tt att act cgt ggt ctc gag att gtg cgc cgt gat tgg agc gaa att gcg aaa gaa act caa gct
G K V/I I T R G L E I V R R D W S E I A K E T Q A

a(g/a)a gtt ctc gag (a/g)ct att ctc aaa cac ggc (g/a)ac gtt gaa gaa gct gtg a(g/a)a att gta aaa gaa gta
R/K V L E T/A I L K H G D/N V E E A V R/K I V K E V

a(t/c)c (c/g)aa aag ctc (g/t)ct aa(a/c) tat gaa att ccg cca gag aag ctc g(t/c)g att tat gag cag att
I/T Q/E K L A/S K/N Y E I P P E K L V/A I Y E Q I

act cgc ccg ctg cat gag tat aag gcg att ggt ccg cac gtg gct gtt gca aag a(g/a)a ctg gct gct a(g/a)a ggc gtg
T R P L H E Y K A I G P H V A V A K R/K L A A K/R G V

aaa (g/a)tt a(g/a)a ccg ggt atg gta att ggc tac att gta ctc cgc ggc gat ggt ccg att agc aa(a/c) cgt gca
K V/I R/K P G M V I G Y I V L R G D G P I S K/N R A

```
att cta gct gag gaa t(t/a)c gat c(c/t)g a(g/a)a aag cac aag tat gac gca gaa tat tac att gag aac cag gtg
 I   L   A   E   E   F/Y     D     P/L     K/R     K   H   K   Y   D   A   E   Y   Y   I   E   N   Q   V
                                                                                  2272 2273

ctc ccg gcg gta ctc cgt att ctg gag g(g/c)t ttt ggc tac cgt aag gaa gac ctc cgc t(a/g)(c/g) caa aag
 L   P   A   V   L   R   I   L   E   G/A     F   G   Y   R   K   E   D   L   R   Y/W/*/C     Q   K

act a(g/a)a cag (g/a)(t/c)t ggc ctc act (g/t)ct tgg ctc aac att aaa aaa tcc ggt acc cac tag tgc tag cat gac
 T   K/R     Q    V/A/I/T    G   L   T    A/S    W   L   N   I   K   K   S   G   T   H   *
```

Figure 9. A comparison of the polymerase to 3' to 5' exonuclease activity

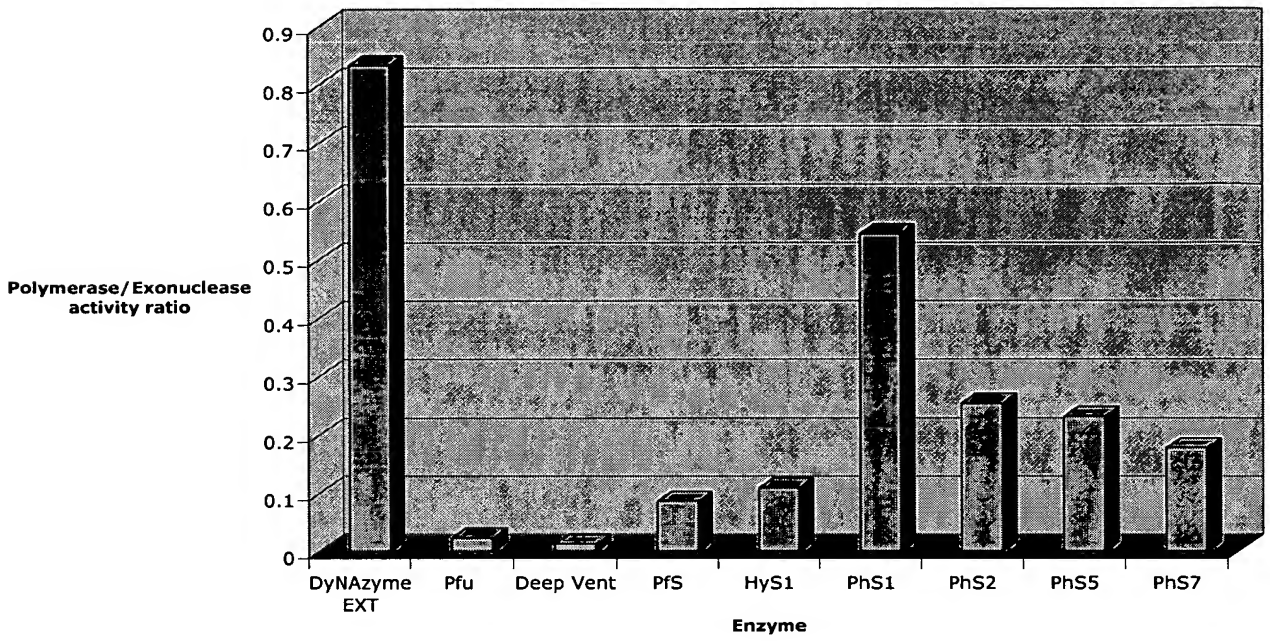


FIGURE 10

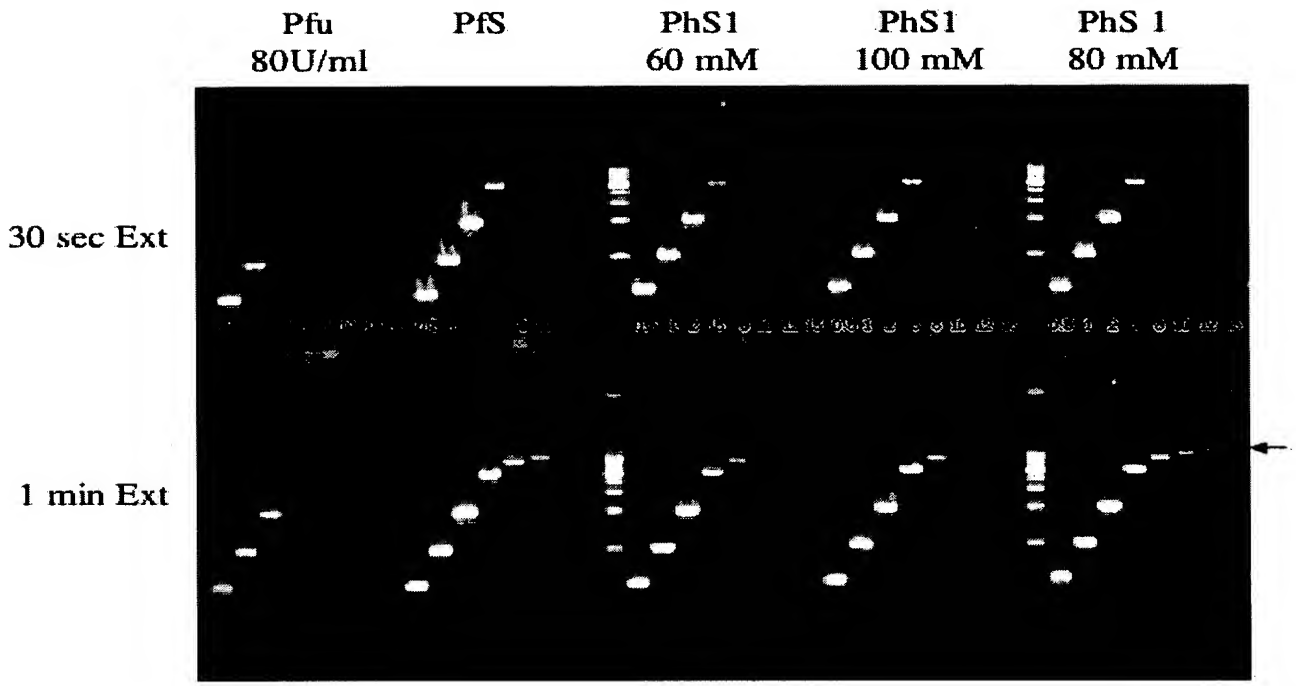
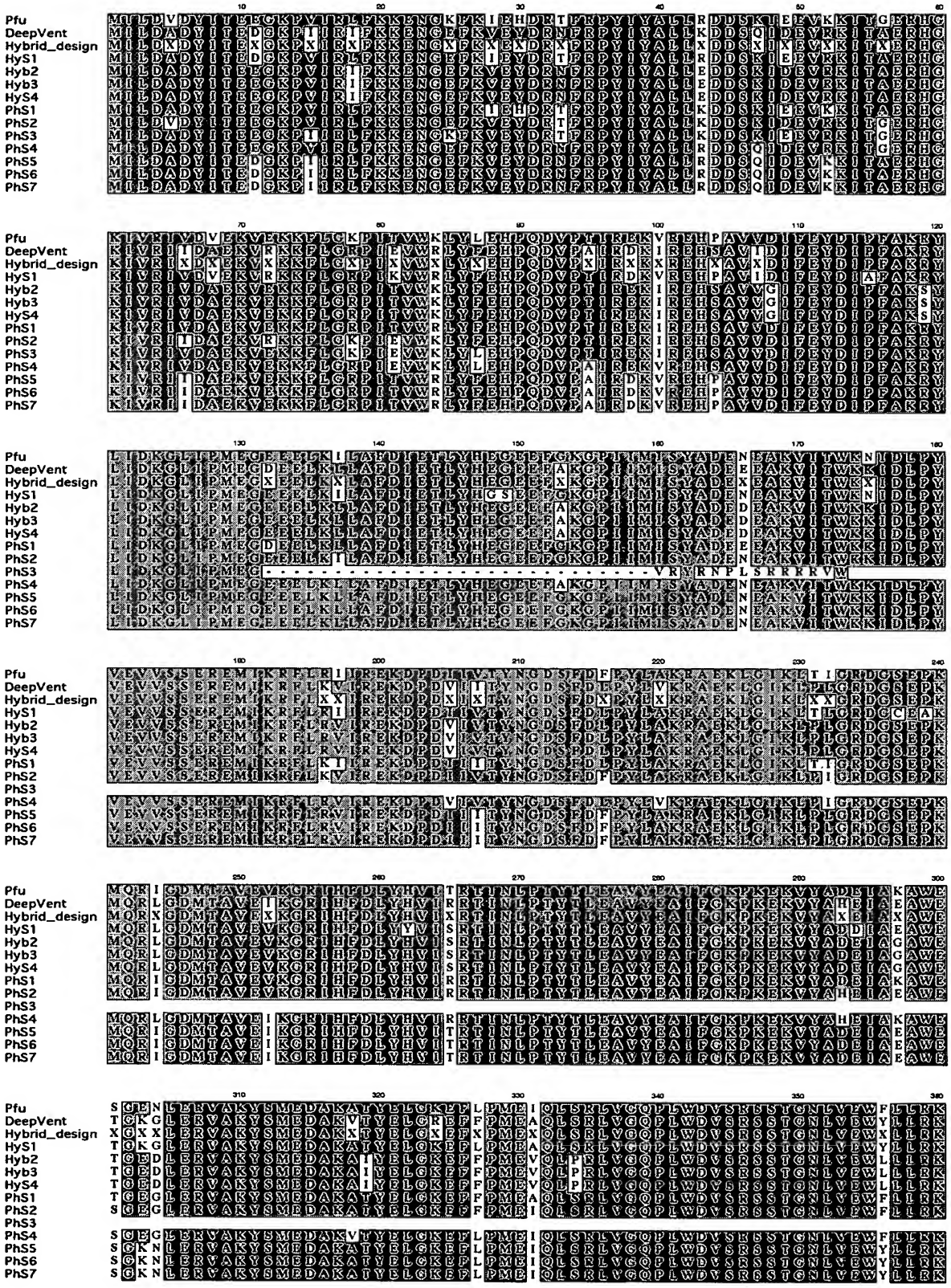
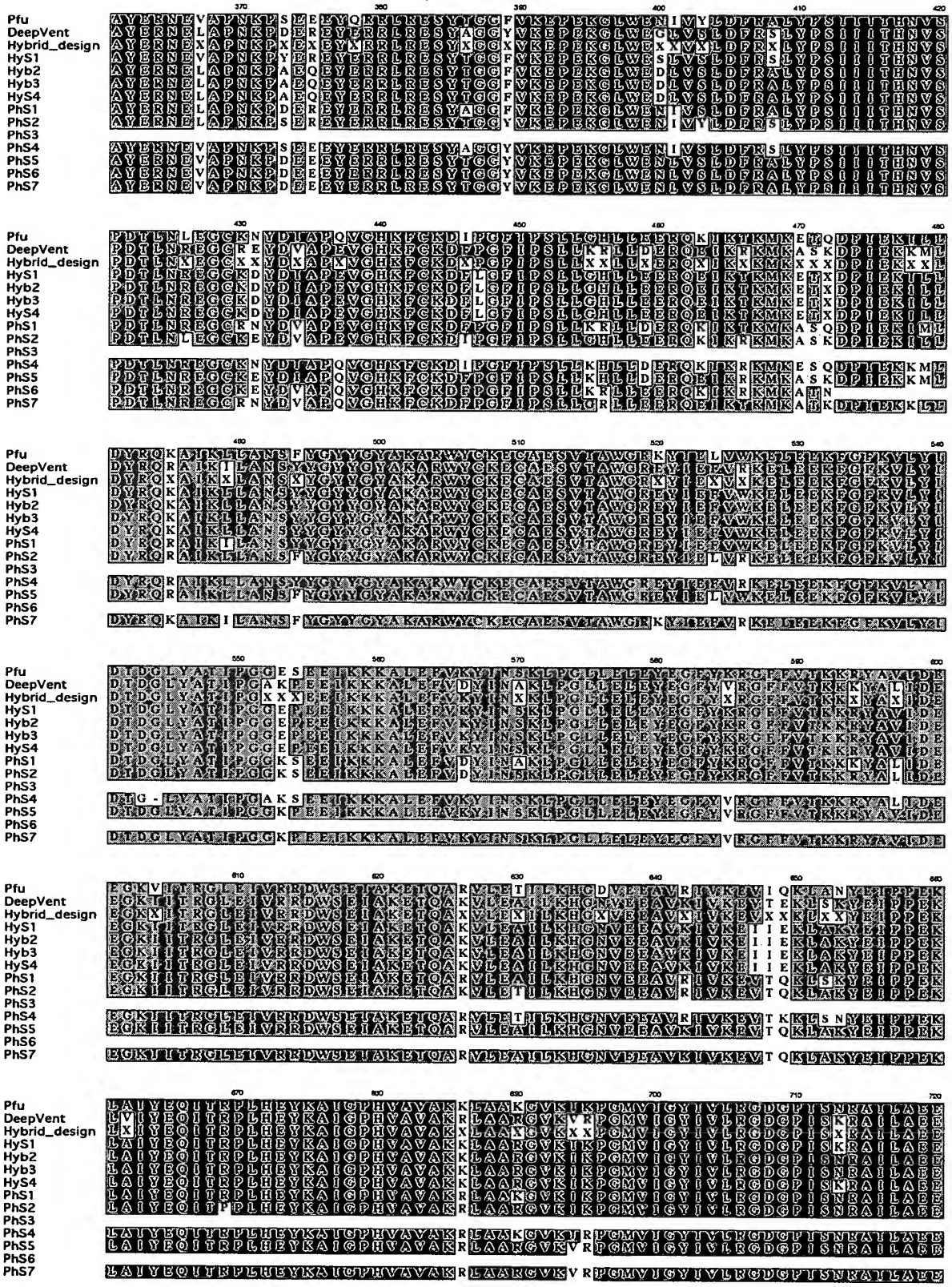
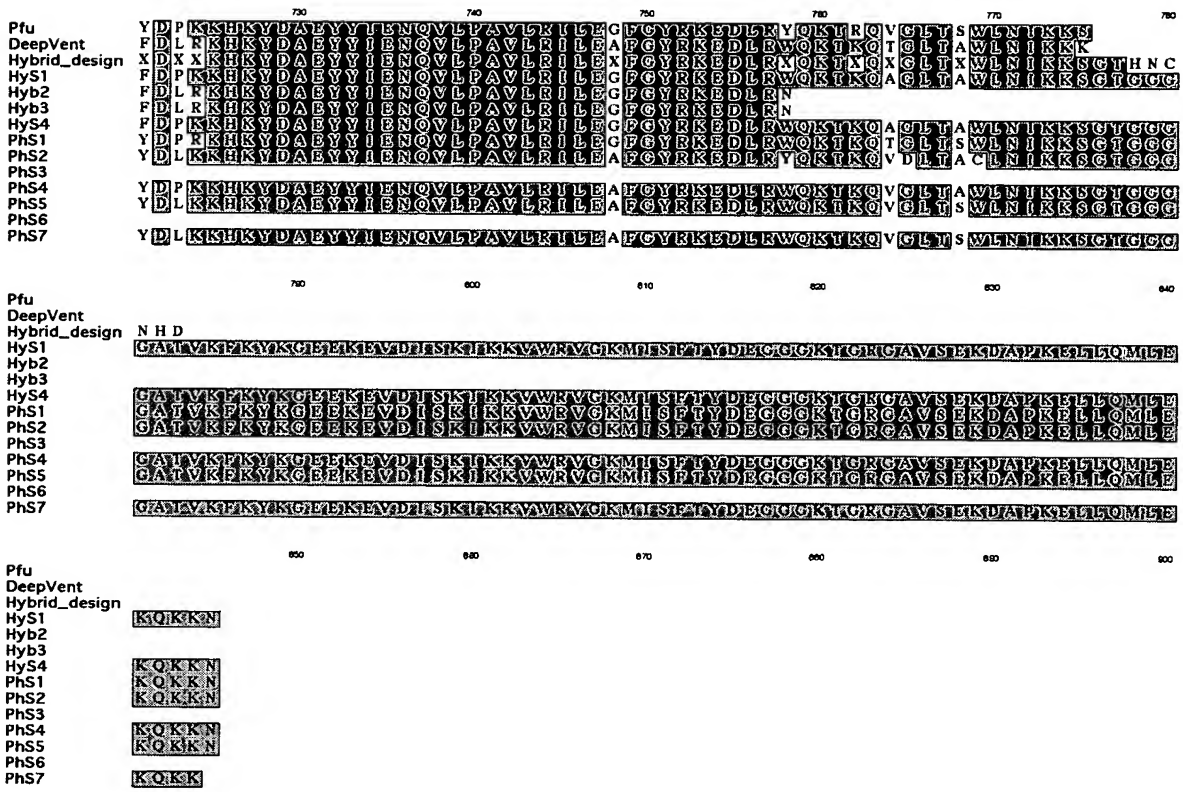

Pfu
80U/ml
PfS
PhS1
60 mM
PhS1
100 mM
PhS 1
80 mM
30 sec Ext
1 min Ext

Figure 11


Pfu
DeepVent
Hybrid_design
HyS1
Hyb2
Hyb3
HyS4
PhS1
PhS2
PhS3
PhS4
PhS5
PhS6
PhS7


Pfu
DeepVent
Hybrid_design
HyS1
Hyb2
Hyb3
HyS4
PhS1
PhS2
PhS3
PhS4
PhS5
PhS6
PhS7


730
740
750
760
770
780
Pfu
DeepVent
Hybrid_design
HyS1
Hyb2
Hyb3
HyS4
PhS1
PhS2
PhS3
PhS4
PhS5
PhS6
PhS7
790
800
810
820
830
840
N H D
850
860
870
880
890
900